```
Results file us-09-497-957-1.res made by tport on Fri 17 Jun 105 17:58:48-PST.
                                                                                                   FastDB - Fast Pairwise Comparison of Sequences Release 5.4
> 0 < O IntelliGenetics > 0 <
```

Query sequence being compared:US-09-497-957-1 (1-10825) Number of sequences searched: 70 Number of scores above cutoff: 70

Results of the initial comparison of US-09-497-957-1 (1-10825) with: File : US09497957.seq

100-

PARAMETERS

30 500 K-tuple Joining penalty Window size 5.00 0.33 Unitary Similarity matrix Mismatch penalty Gap penalty Gap size penalty Cutoff score Randomization group

SEARCH STATISTICS

Scores:

Standard Deviation 1325.40 Total Elapsed 00:00:01.00 Median 19 51359 70 70 CPU 00:00:00.08 Mean 232 Times:

Number of residues: Number of sequences searched: Number of scores above cutoff:

A 100% identical sequence to the query sequence was found: The scores below are sorted by initial score. Significance is calculated based on initial score.

Sequence Name

Init. Opt. Length Score Score Sig. Frame Description

	The list of other best scores is: Init. Opt. Sequence Name Description Length Score Stg. Fram
--	---

1730   1740   1750   1760   1770   1780   1790   1800   CTGTTCAAGCCCCAAGGGAAACAAGTCTTTACCCTTTGATATTTTGCATTCTAGTGGGAGA   1791   1   1   1   1   1   1   1   1   1	1810 1820 1840 1850 1850 1870 GATGACAATAAGCAGAAAGAATACAACATCAGGAAATATGGCTGTTGTGAGAAGCAGAAAGAA	1880 1890 1900 1910 1920 1930 1940 TCAGGGCAAGTCACTCTGGGGCTGACATGAGGAAATAAGAATGATTGACTGGGAG	1950 1960 2010 CAGTATTTCCCAGGCAACTGAGCCTGGCAAGTTGGATTAAAAAGCGGGTTTTCTCAGACTACTCAT	2020 2030 2040 2050 2060 2070 2080 GTGTGTGTGTGTGTGGGGGGGGGGGGGGGGGGGGGG	2090 2100 2110 2120 2130 2140 2150 2160 GCAGTATCTGTCTCTCTCTTGTCTTCTCTCTTGTCTTGT	2170 2180 2190 2200 2210 2220 2230  AAACTTTGCCACATGTCACCTAGTAGAACCAACTTAGGTTTAAGAAGTTCGGGTTTGAAAAAAAA	2240 2250 2260 2270 2280 2290 2300 2300 2300 2300 2300 2300 230	2310 2320 2370 CCTGTAGGCTGGTGTGAATTCTAGCCAAGGAGTAACAGGTGAACAGGCTTTTAAAAGATTGCTCT	2380 2390 2400 2410 2420 2430 2440
1590   1600   1610   1620   1630   1640   1650   1650   1671   1671   1771   1772   1773	1590   1600   1610   1620   1630   1640	1590   1600   1610   1620   1630   1640	1590   1600   1610   1620   1630   1640	1590   1600   1610   1620   1630   1640	1590   1600   1610   1620   1630   1640	1590	1590   1600   1610   1710   1610   1710   1610   1710	1550   1600   1610   1620   1630   1640   1650   1640   1650   1650   1640   1650   1700   1710   1710   1700   1710   1700   1710   1700   1710   1700   1710   1700   1710   1700   1710   1700   1710   1700   1710   1700   1710   1700   1710   1700   1710   1700   1710   1700   1710   1700   1710   1700	1590   1600   1610
1690	160	1660   1670   1680   1690   1700   1710	1660   1670   1680   1690   1700   1710	1660   1670   1680   1690   1700   1710     ATAATAAAATTTCATGTTGAGCAGAAATTCATTGTTTACAAGTGTAAATGAGTCCCAAGTGATAAATGAGTCCCAAGTGAAATTCATGTTGAGCAGAAATTTCATTGTTTACAAGTGTAAATGAGTCCCAAGAATTCATGATTCATGATTCATGATTCATGATTTTACAGTTAAATTTCCCAAGGAGAAGAAGAACAGAACAGTGTTAACCCTTTGATATTTTGCATTTTACAGCCCCAAGGAGAAGAAGAACAAGTCTTTACCCTTTGATATTTTGCATTTTTCCAAGCCCCAAGGAGAAGAACAACAAGTCTTTACCCTTTGATATTTTGCATTTTTTCCAAGACAAAAACAACAACAACAGGAAAACAATCAGGAAAAAAAA	1660   1670   1680   1690   1700   1710     ATRATAAATTTCATGTTGAGCAGAAATTTCATTGTTTACAAGTGTAAATGAGTCCCAAGTGATAAAATTTCATGTTGAGCAGAAATATTCATTGTTTACAAGTGTAAATGAGTCCCAAGAATTTCATGTTGAGCAGAAATATTCATTGTTTACAAGTGTAAATGAGTCCCAAGAGTGTAAATGAGTCCCAAGAGTGTAAATGAGTCCCAAGAGTGTAAATGAGTCCCAAGAGTGTAAATTTTCACAGTTCAAGCCCCAAGGAGAAGAGAACAAGTCTTTACCCTTTGATATTTTGCATTTTTCAAGCCCCAAGGAGAAGAGACAGAACAACAGGAAACAATCAGGAAAACAATTACAATTTTTCAAGCCCCAAGAGAAAGAA	150	ATASTADANTTICATION 1680 1690 1700 1710 ATASTADANTTICATION 1680 1690 1700 1710 1710 1710 1710 1710 1710 17	150	1500   1670   1680   1710
	1740	T30 1740 1750 1760 1770 1780 1780 1780 1780 1780 1780 178	CTGTTCAAGCCCCAAGGAGAGAGAAACAAGTCTTTACCCTTTGATATTTTGCA   CTGTTCAAGCCCCAAGGAGAGAGAGAGAACAAGTCTTTACCCTTTGATATTTTGCA   CTGTTCAAGCCCCCAAGGAGAGAGAGAGACAACAAGTCTTTACCCTTTGATATTTTGCA   170	T30 1740 1750 1760 1770 1780 1780 1780 1780 1780 1780 178	TGGGGCAAGGGGGGAACCAGGGAAACCAGTTTACCCTTTGGTATTTTGCAAGCCCCAAGGGGAAGCAGGGAAACCAGTTTACCCTTTGATATTTTGCAAGCCCCAAGGGGAAGCAGGGGAACCAGTCTTTACCCTTTGATATTTTGCAAGCCCCAAGGCGAAGCAGGGGAACCAGTCTTTACCCTTTGATATTTTGCAAAACCAAAACACCCCAAGGCGAAACCAGCGGAACCAGTCTTACCCTTTGATATTTTGCAAAAACCAAAAACAAAACAAAAACAAAAAAAA	CTGTTCAAGCCCCAAGGAGAGAGACAAGCAATTAACCCTTTGATATTTTGCAAGCCCCAAGGCGAAGACAGGAAACAAGTCTTTAACCCTTTGATATTTTGCAAGCCCCAAGGCGAAGACAGGCGAAACAGTCTTTAACCCTTTGATATTTTGCAAGCCCCCAAGGCGAAGACAGTCTTTAACCCTTTGATATTTTGCAATTCAAGCCCCCAAGGCGAAACAACAGTCTTTAACCTTTGATTTTTGCAATTAAGCAAATGACAGAAAACAATCAGGAAATCATGGGTGTTGTGGATGACAATAAGCAAAAGAGAAATAAGCAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAAAGAAAA	Transcreeceaaggagagagagagagagagagagagagagagagag	CTGTTCAAGCCCCAAGGAAACAGCTTTTTTTTTTTCAAGCCCCAAGGAAACAGCTTTTTTTT	1740

Control   Cont	3250 3260 3270 3280 3290 3310 ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGAATCCCTTGAACCCAGGAGGTGCAGTGCAGTGAGTG
--	---

σ, ,	S350 S370 S370 S370 S370 S370 S370 CAATGCAATAAAGGGCAATTTTATCTATCAAAAAAACGGTAACGATAATTTAAATGTG [	CCASTCTTCCTGGCAAGGGTAAACAGTCCCTCTCTCTCTTTCCTGTTCCTGTCTTTCTT
### AGENCYTGAGGCAGCAGCAACAAGGAATTTGCTTCCTGAGATCATTTGGTCCTTGGGGAT ###############################	### 470 ### 4480 ### 450 ### 4520 ### 4530 #### 4530 #### 4530 #### 4530 #### 4530 #### 4530 #### 4530 #### 4530 #### 4530 ##### 4530 ####################################	

2011-13	2-2 t-t 2-2	H-H 09-90 Y-V	<u> </u>
5970	### 1990   1990		10 6620 3GTTGAAGATGGG 3GTTGAAGATGATGGG 10 6620 3ATTAGAAATAATTAC [
AGCTGAGAAAATCTATTGGGGGTTGAGGGGGTGAAATTATGGCAGTGAGAAGATCTGC	TGTTCALAISO	AACATCTTCAGAGCACCTACTATTTGCAAGAGCTGTTTAAGGTAGGT	6550   6570   6580   6590   6600   6610   6620
10 5950 11	6160 6160 6160 6160 6160 6230 7769CATCCATG 7769CATCCATG 7769CATCCATG 7730 7769CATCCATG 7769CATCCATG 7769CATCCATG 7769CATCCATG 7769CATCCATG 7769CATCCATG 7769CATCCATG 7769CATCCTC 7769CATCTC 7769CATCCTC 7769CATCCT 7769CATCT 7769C	TGTTTAAGGTA( TGTTTAAGGTAA  6450 6450 6450 6450 6450 6520 6520 6520	1590   660   1590   1
930 1940 1940 1940 1950 1	CAGGGTTCAACT CAGGGTTCAACT CAGGGTTCAACT 6150 6220 6CAGGGGGATC 6220 6320 6340 6GAGAGAGAAAA CAGGAAAAAAAAAAAAAAAAAAAAAA	TTTTGCAAGAGC TTTTTGCAAGAGC 6370 6440 AAATCTGGTAGG AAATCTGGTAGG AAATCTGGTAGG CAGGAAGCAAAT 6510 GGGAAGCAAAT CAGGAAGCAAAT CAGGAAGCAAAT	6560   6590   6690   6990
5920 5920 5920 5920 5920 5920 600 600 600 600 600 600 600 6	5140 TTAAGGAAAAGG TTAAGGAAAAGG 6210 6210 TTGGAAAAAGGG 6210 6210 6210 6210 6210 6210 6210 6210	AGCACCTACTA AGCACCTACTA AGCACCTACTA 50 6430 TCTCAGAACCC   	6570
5910 AGCTGAGAAAA [           AGCTGAGAAAA 5910 5980 5980 1CTTTGTTAGGG 5980 5980 6060 CGTCTGGCACCC CGTCTGGCACCCC CGTCTGGCACCCC CGTCTGGCACCCC CGTCTGGCACCCCCCCCCC	TGTTCATALIA 	AAACATCTTCAGAGCACCTACTATTTTGCAAGAGCTGTTTAAGGT 	6560 TOGGGATCAAGI

570 7580 7590 7600 7610 7620 763 7 7650 7670 7670 7680 7690 7700
7570 7580 7630 7600 7610 7620 7630  AACCITACAGAITITIAAACAIGIAICHIIIIIIIIIIIIIIIIIIIIIIIIIII
7490 7500 7510 7520 7530 7540 7550 7560  AAAITIGGGGGACTIACAITITIAACAICIGAGAAAAGCTITIGAACCCTGGGACGTGGCTAGTCAT
7420 7430 7440 7450 7460 7470 7480 TTCATTTCCTCCGTCACCTCAGACATACCCTAGTTTTCATTTTTGAAGAGACTCCTTTTTTTT
7350 7410 CGGTGATCCCTAGCTGTGACCTCTCCTCTCATGAACCTCCAAGCTGCATCTAGAGGCTTCC
7280 7330 7340  CCTTGATTTTAGCCTTCTCTTCATTTCCTCAAAAGATTTCCCCATTTAGGTTTCTGAGTTCCTGCTAGC
7210 7210 7220 7270 7270 7270 7270 7270
7130 7140 7150 7200 7200 7200 7200 7200 7200 7200 72
7060 7100 7120 ATGGTGCCTAGGTTTGTGTATCCTGGGTCTCTTGTCTCACAGAGGAGCCATGGGGACTACGT
6990 7000 7010 7020 7030 7040 7050 TGAAATCCAAGTCAAATTCAAGTCAAATTCAAGTCAATCAA
6920   6930   6940   6950   6960   6970   6980
6850 6860 6910  TCACTIGGGGTIGTCATTGAAGGATCCTAAGAAAGGAGGACCACGATCTCCCTTAATAGGTGAATGTTTTATTGTTTATTGTTTTTTTT
6770 6780 6790 6800 6810 6620 6830 6840 GTAGGGAAAGAGAACCAGCTCATACAGAGCCCAGGGTCTTTTGGGATATTGGGTATAGA GTAGGGAAAAGAGAATCAGAAAGAGCCAGCTCATACAGGGTCTTTTGGGATATTGGGTATAGA

		8860   8870   8880   8890   8900   8910   8920   8920   8920   8920   8920   8920   8920   8920   8920   8920   8920   8920   8920   8920   8920   8920   8930   8030   8930	9010   9020   9030   9040   9050   9060   9070	9150 9160 9170 9180 9190 9210  CCCAGGTTCAAGCGATTCTCCTGTCTCCCAAGTAGCTGGGATTACAGGCGTGCACCATGCCCG	9220 9230 9340 9340 9350 9360 9290 9300 9310 9320 9330 9340 9350 9360 TCGTGATCCGCCTGCCTCCGAAAGTGCTGAGATTACAGGTGTGAGCCCCCTCCCT
TCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTCCATCTGATTGTGATGTGAGTTGCA   TCTGTGTTACCCAGTAACTCATCTGTCACCAAGCCTTGGGGATTCTTCCATCTGTGTGTG	GGTAGTARTGATGGGTGGTAGGAGGCAAATAATCTTGAAAGGGGTTGTAGAAGAGGTGTTTTTC GGTAGTAGTAGTAGTAGTAGGAGGCAAATAATCTTGAAGGGGTTGTAGAAGAGGTGTTTTTC GGTAGTATGATGATGTTTTTAGCAGGTAGGAGGCAAATATCTTGAAGAGGGGTTTTTTTC 7780 7790 7810 7810 7820 7820 7840 7840  TAATTGGCATGAAGGTGTCATAAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT TAATTGGCATGAAGGTGTCATAAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT TAATTGGCATGAAGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTACTCTAGTAT TAATTGGCATGAAGGTGTCATACAGATTTGCAAAGTTTAATGGTGCCTTCATTTGGGATGCTTACTTA	1930   7940   7950   7960   7970   7980   8000   8010   8020   8030   8040   8050   8050   8040   8050   8050   8040   8050   8050   8040   8050   8040   8050	8070   8080   8090   8100   8110   8120   8140   8150   8160   8170   8180   8190   820   820   8200   82	8210   8220   8230   8240   8250   8260   8270   8280   8290   8310   8320   8330   8340   8350   8290   8310	TGAGCCGAGTTTGCGCCACTGCACTCAGGTGACAGACTCAACTCAAAAAATAAAATAAAATAAAAATAAAATAAAATAAAATAAAA

ATATATATATCAGATGGCATGTGTTTACTTTATGTTACTACATGCACTTGGCTGCATAAATG 00 9380 9390 9400 9400	9440 9450 9460 9470 9480 9490 9500 TGGTACACACATCTGTCTTGACGATACCATACACATACACACAC	9510 9520 9530 9540 9550 9560 9570 GGATTAAATTTTAGGAAAGATATCTTCTTTTATTTTGTGGTTAGAAAGTTA	9580 9590 9600 9610 9620 9630 9640 TGTRGAAAAAGTAAATGACATTTACCCTCATTGTACAAAAGCTATAAAATGAATAAACCTGTTAT	50   9660   9670   9680   9690   9700   9710   9720   97	9730 9740 9750 9760 9770 9780 9790  TATACTITAATAAATGTATATTGTATACTGGATGATTTTATTGAAGTTCTTGTTCATCTTGTGTATA	9800 ; 9810 9820 9830 9840 TACTTAATCGCTTTGTCATTTTGGAGACATTTATTTTGCTTCTTAATTTTGTTTTTGTCTTAGGAATA	9870 9880 9890 9900 9910 9920 TITICATICAACIGIGAGCGAATIAATGGTTTCTTCACTCAGGGACATIGICGTCTAAGTTGTAAGTGTAAGTTGTAAGTTGTAAGTTGTAAGTTGTAAGTTGTAAGTTGTAAGTTGTAAGTTGTAAGTGTAAGTAGT	9940 9950 9960 9970 9980 9990 10000 ACATTGGTTAITTACCAGCAAACCAITCTGAAAGCAIATGACAAATTAITTCTCTTTAIATATCTTAATA	010         10020         10030         10040         10050         10060         10070         10080           ACTGAAAGCAGACTGCTATACTCTTCTACCTCATAAGGAATATGTTACAATTAATT	10090 10100 10110 10120 10130 10140 10150 AGGTAAGCATTTGTTTTTATTTTCACCTGGGCTGAGATTTCAAGAAAACACCCCAGTCTTCACA	10160 10170 10180 10190 10200 10210 10220 GTAACACATTTCACTAACATTTACTAACATCAGCAACTGTGGCCTGTTAATTTTTTTAATAGAAATTTT	10230 10240 10250 10260 10270 10280 10290 AASTCCTCATTTTCTGGGGTTTTTTTTTTGGGCTTTATTCTTATAGGTCAAC
AGAGTCTTAATATATATATC 9370 9380	9440 945 TGGTACAAGCATTCTGT                 TGGTACAAGCATTCTGT 9440 945	9510 9520 GCATTAAATTTTAGCAA 	9580 9590 TGTAGAAAAAGTAAAI               TGTAGAAAAAGTAAAI 9580 9590	9650 TTAATTAGCCAGTGAAA                TAATTAGCCAGTGAAA 9650	9730 TATACTTTAATAATGT             TATACTTTAATAAATGT 9730	9800   981 TACTTAATCGCTTIGTC               TACTTAATCGCTTTGTC 9800   981	9870 9880 TTTTCATTCAACTGTGG	9940 9950 ACATTGGTTALTTACC 	0010 10020 ACTGAAAGCAGACTGCT               ACTGAAAGCAGACTGCT 0010 10020	10090 AGGTAAGCATTIGITITI 	10160 1017 GTAACACATTCACTAA 	10230 AAGTCCTCATTTCTTT 

10270 10280 10290	10340 10350 10360 TTATTCACCTCTGGCAAACCATTCACAAACCATTGG [	10410 10420 10430 10440 AANGTACCACGGGGGCCCGGTGACCAGACAGGCGGGGGGAAAAAATGACCACGGTCGTCGGTCG	10450 10460 10470 10480 10490 10500 10510 CTGAGGGTTTTCCTGAAGGTAAAGAATAAAGAATGGGTGGAGGGGGTGCACTGGAAATCACTTGTAGA	10520 10530 10540 10550 10560 10570 10580 GAAAAGCCCCTGAAAATTTGAGAAAAAAAAAAATAACTTAACCAGCTATTTGAATTGCTCGAATCACAG	10590   10600   10610   10620   10630   10640   10650   10640   1065	0660         10670         10720           GTACAGCAGGTGATTGAGGGTACAGGCCAAAATTCTTATGTTGTATATATA	30		on US/09497957	re = 10824 Significance = 7.99 = 10824 Mismatches = 1 Substitutions = 0	X TCTAAGGTTGAGATAAATTTTTAAATGATTGATTTTGAAATCATAATATTTTAAATATCTAAAGT TCTAAGGTTGAGATTAAATTTTTTAAATGATTGATTTTTTTT	80 90 100 110 120 130 140 CAGATCAGAACATTGCCCAATCAACACCCCTTCAGGATTTAAAAACCAAGGGGA [	150 160 210 210 210 190 200 200 210 CATGGGAGAGAGAGAGAGAGAACTFACTGAAAGA (HILIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII
10260	10330 TTTAAATTC          TTTAAATTC 10330	10400 GCCATAGGT          GCCATAGGT 10400	470 AATAAAGAA          AATAAAGAA	0 AAACAAGAA          AAACAAGAA	10620 ACACAACAG          ACACAACAG	10690 GAGGTACAG          GAGGTACAG 10690	CATTCTTCA CATTCTTCA           CATTCTTCA		Application	Optimized Score Matches Conservative Sul	30 GTATGATTG GTATGATTG 30	TCCCCAATC TCCCCAATC TCCCCAATC	180 AGGTACCTT
10250	10320 AGACCTGCAT          AGACCTGCAT 10320	10390 ACACCTGGTG          ACACCTGGTG	460 10 AAGGTAAAGG           AAGGTAAAGG	0 TTGAGAAAAC           TTGAGAAAC	10610 TGAACTGGGA          TGAACTGGA	10680 GGACTGCTGA           GGACTGCTGA 10680	10750 TTTTATAAAA TTTTATAAAA 10750	820 X TCATAAAC         TCATAAAC 820 X	-10825) quence 5,	0824 Opti 99% Matc 0 Cons	20 ATTTTAAAT           ATTTTAAAT	GAAGCTACTT GAAGCTACTT GAAGCTACTT	170 TTTCACAAGC
10240	10310 10320 10330 10340 TGAAAATCAAAGACCTGCATTTTAAATTCTTATTCACTTATCACTTCACTTTAAAATTCTTATTCACTTTTAAAATTCTTATTCACTTAAATTCTTATTCACTTAAATTCTTATTCACTTAAATTCTTAATTCACTTAAATTCACTAATTCACTAATTCACTAATTCACTAATTCACTAATTCACTAATTCACTAA	10380 10390 10410 GAGAAGGGGAAACCTGGTGGCCATAGGTAAATGTAC 	450 10 GGTTTTCCTG          GGTTTTCCTG	1053 CCCTGAAAAT           CCCTGAAAT 0 1053	10600 CTGAGCTGCC           CTGAGCTGCC	10670 AGGTGATTGA           AGGTGATTGA 10670	10740 ACTGTCAGTA           ACTGTCAGTA	810 10820 X CCCAAATTTTCATAAAC [             CCCAAATTTTCATAAAC 810 10820 X	7-957-1 (1. 7-957-5 Sec	ore = 1 entity =	10 TTGAGATAAA            TTGAGATAAA	AGAACATTGC           AGAACATTGC	160 rcaccragrg
10230	10300 TACALTTC         TACALTTC	10370 TAGTAAAG                   TAGTAAAG	CGCTGAGG	1052 GADAGG         GADAAGG	10590 GCCATTG        GCCATTG	10660 GTACAGC         GTACAGC 10660	10730 TTATAAT7                 TTATAAT7	108: TAAAATCCC         TAAAATCCC	2. US-09-49' US-09-49'	Initial Sco Residue Ider Gaps	X TCTAAGG' TCTAAGG' X	1CAGATCJ TCAGATCJ TCAGATCJ TCAGATCJ 8(8)	150 CACTGGA

1010   1020   1030   1040   1150   1160   1070   1080   1070   1080   1090   1090   1100   1110	CIGTTCAGGGAGAGAGAGAGAGAGACAGGGAACAACAGILIIIIIIIIII
Cartegarical Control And Con	AGAAGGCTGAGCAAACCCACGAGGATTCCGCCACCGAATGCATTGGGGGGTGGG

1950	2090   2100   2110   2120   2130   2140   2150   2160     GCAGTATCCTGTCCTACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAAAATGTCTCT   GLAGATACCTGTCCTCCTACTAGGTGCTAGGAGCACTCCCCCAGTCTTGACAAAATGTCTCT   GCAGTATCCTGTCTCCTCACTAGGTGCTAGGAGCACTCCCCCAGACTCTTGACAAAAATGTCTCT   GCAGTATCCTGTTGCTACTAGTAGGTGCTGGGACTCCCCCAGACTCTTGACAAAAAATGTCTCT   2090   2170   2180   2190   2200   2210   2220   2300     AAACTTGCCACATGTCACTAGTAGACAAACTCCTGGTTAAGAAGGTCGGGTTGAAAAAAATAAAAAGTA	2240 2250 2260 2270 2280 2390 2300 GTGCTGGGGAGTAGAGGAGCTAGTGAGGAGCCCCCAAACAAGGAGCCCGCAAACGAGGCGCGGGGGG	2380 2390 2400 2410 2420 2430 2440 GGCTGCTATGTGGAAAGGAGGAGCAACGTAAAAGCAGGGGGCCCAGCCAG	2530 2540 2550 2560 2570 2580 2590 TATATTCTGAAGGAAGTTGCTGAGGATTCTATGTTGTGAGAGAAAAAAGAAATTGGCTGGGTGTAGTA	2600 2610 2620 2630 2640 2650 2660 GCTCATGCCAAGAAGAAGAAATTCCTGAGCTTCAAGAACAAGACAACAC	AGCADACCCCTTOTTACADADADATAGCTGGGGTGTGGGGCGCGCTGTGATCCTAGCTA 	2740 2750 2760 2776  CTCGGGAGGCTGAGGTGAGGCCAGGAAGTTGAGGCTGAGCCATGACTGTGCCA  CTCGGGAGGCTGAGGTGAGG
------	---	--	---	---	--	---	--

Transport   Tran	2850 CTGTCTCCCTGACCCCTG 2850 2850 2850 2850 2850 2850 2850 2850	2860 GACCCCCTGAAAAAC 2860 2930 2930 2930 2930 2930 2930 2930 293	CGARGCAAGACCTCTCTCCCTCACACCCCTCAAAAAAGAGTTAAAGT	### ### ### #### #####################
;	3640	3650	3660 3670	
3680 3690 3700	3710	3720	3730 3740	

	TGGGAGGCCACAATCATGGGTTAA 4690 470 4760 4770 CTTGCTTTTATTTAACCAATAATCTTTTTTTTTTTAACCAATAAT	4900 GACCAGCCTGACCAACATGATGAAACC	S050   S050   GCCAAGATCGCGCCACTGCACTCCAG	5190 5200 5210 AGTAGAACAATCCTTTAGGTTAAAAGI 	
GATGGTATGAGTTGATGCAGGTGTGGAGGCTCAACATCCTGCTCCCTACTACACATGGTTAAGGCC	TTCCTTGTTTGAAGCTTTGGGCTACGTGGTGGTGTTCTATGATGATGAGGGGCGGGTGTGGGCCGTGTTGTTGTTGTTGATGAGGGGCCGTGTGGGCCGTGTTGTTGTTGATGATGAGGGCCGGGTGTGGCCGTGTTGTTGTTGATGATGAGGGCCGGTGTTGGGCGGGGTGTGGGCCGGGGGGGG	4040   4050   4060   4070   4080   4020   4030	4180 4190 4200 4210 4220 4230 4240  GGTGGAAATAGGGACTATTCCTTTGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACCCTG  GGTGGAAATAGGGACTATTCCTTTGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACCCTG  GGTGGAAATAGGGACTATTCCTTTGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACACCTG  4180 4200 4210 4220 4220 4230 4230  CAGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAGTACCGAGGGCTACTGGAAGTACGGGTATGATGGG  CAGGTCATCCTGGGCTGTGAAATGCAAGAAGACAACAAGTACCGAGGGCTACTGGAAGTACGGGGTATGATGGG  CAGGTCATCCTGGGGCTGTGAAATGCAAGAAGACAACAAGTACCGAGGGCTACTGGAAGTACGGGGTATGATGGG  CAGGTCATCCTGGGGCTGTGAAATGCAAGAAGACAACAAGTACCGAGGGCTACTGGGGGTATGATGGG	4250 4250 4320 4250 4350 4350 4370 4380 4390 4390 4390 4390 4390 4390 4390 439	CTGGAGTGGGAAAGGCACAAGATTCGGGCCAGAACAGGGCCTACCTGGAGAGGGACTGCCCTGCACAG CTGGAGTGGGAAAGGCACAAGATTCGGGCCAGGAGCGACCTACCT

						S900 673   GAGAGCAGG   TGTACCTTAACCC 	· · · · · · · · · · · · · · · · · · ·	TCAC TCAC	A A A	6990 TGANATCCAN 	7060 ATGGTGCC               ATGTGCC 7060	7130 7140 CTARTCARC CTARGCTGARCGT
AGGAGAACAAGCTGACTGCTCTCCAAGTGACACTGTGTTAGGGTCCAATCTTAGGACACAAAATGGT 5410 5420 5430 5440 5450 5470	5480 5540 5540  5540  GTCTCCTGTAGCTTGTTTTTTCTGAAAGGGTATTCCTTCC	S550   S560   S570   S580   CCAGTCTTCCTGGCAAACAGATCCCTCTCCTCTTCCTCTTTGTCAAACAGATCCCTCTCTCT	5620   5630   5640   5650   5660   5670   5680   GRAAGGTGACCATGACTACCACCCCAGGGTGACACATGACTACTACCCCCAGGGTGACACATGACTACACTACACAGGGTGACACATGACACATGACACATGACACATGACACATGACACATGACACACAC	5690         5700         5710         5720         5740         5750         5760           AACATCACCATGAAGGGTGAAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCGAACCTAAAAGCAGGTATTG	5770 5820 5830 5830 5830 5810 5820 5830 5830 58310 5830 5830 5830 5830 5830 5830 5830 583	5840   5850   5860   5870   5880   5890   5900   5800   5890   5900   5800   5890   5890   5890   5890   5890   5890   5890   5890   5890   5880   5880   5890   5800	5910         5920         5920         5970           AGCTGAGAAAATTATGGCGTTGAGGAGTGCTGAGGAGGTAATTATGGCAGTGAGATGAGGATTCTGC	5980   5990   6000   6010   6020   6030   6040   TCTTTGTTAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	6050   6060   6070   6080   6090   6100   6110   6120   CGTCTGGCACCCTAGTCATCAGGAATTT	6130 6140 6150 6160 6170 6180 6190 TGTTCATAATATTAAGGAAGGCAGGGTTCAAGTGAGTGAG	6200 6210 6220 6230 6240 6250 6260 CCCAGGGCACCACGGCACCATTTTCTCATTTATATTCTCATTTATATTCT CCAGGGCACACGCACACACATTTTTCTCATTTATATTCT CCAGGCACACACACACACACACACACACACACACACACA	6270 6280 6330 6330 6310 6320 6330 TTGGGGACACCAGGAGCTCCCCTGGGAGAAAATAATGGTTCTCCCCAGAATGAAAGTCTCTAATTCAAC 

6270 6280 6290 6300 6310 6320 6330	6340 6350 6360 6370 6380 6390 6400  AAACATCTTCAGAGCACTATTTTGCAAGAGCTGTTTAAGGTACTACAGGGGCTTTGAGGAAGT	6410 6420 6430 6440 6450 6460 6470 6480  CACTGTGGCTATTCTCAGAACCCAAATCTGGTAGGAATGAAATTGATAGCAAGTAAATGTAAAGAAG  [	6490 6550 6550 6550 6550 6550 6550 6550 65	6560 6570 6580 6590 6600 6610 6620 TGGGATCAAGATAGCTTTGAAGAGAAGCTGGATTCCATTAGGTGAGGTTGAAGATGGG	6630 6640 6650 6660 6670 6680 6690 AGGICTACACAGGAGCAACCAGGAGGAGGAGAGGCATACTGGGAGATTAGAAATAAC	6700 6710 6720 6730 6740 6750 6750 6760  IGTACCTTAACCCTGAGTTTGCGTAGCTATCACTCACTTATGCATTTCTACCCCCTGAACATCTGTGGT	6770 6780 6830 6840 GTAGGGAAAAGAGAATCAGAAAGACAGCCCATACAGAGTCCCAAGGCTCTTTTGGGAAATTGGGTTATGA	6850 6860 6870 6880 6890 6900 6910 TCACTGGGGTGTCATTGAAGAACGAGGACCACGATCTCCCTTATATGGTGAATGTGTTTA	6920 6930 6980 AGAAGTTAGATGAGAGAGAGACAGTTAGAAAGCCATTAGATTTCCAGATGAGAGATAAYCGTTCT	6990 7080 7010 7020 7030 7040 7050 7050 TGAAATCCAATAGCCAAGGCAAGGCAAGGCAAGGCAAGG	7060 7120 7120 7120 7100 7100 7110 7120 7100 7110 7120 712	7130 7140 7150 7160 7170 7180 7280 CTTAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG
------------------------------------	---	---	--	---	--	--	--	---	--	---	--	---

8070 CAATAA        CAATAA 8070	8140 8150 8160 8170 8180 8190 8200 ACCGTGGCTGATAATCCCAGCACTTTTGGCAGGCTGGATGGA	8210   8220   8230   8240   8250   8260   8270   8280   8280   8270   8280   8280   8270   8280   8280   8270   8280   8280   8280   8280   8220   8230   8240   8250   8250   8280	8350   8350	8360   8370   8380   8400   8410   8420   19	8430         8440         8450         8460         8470         8480         8490           AAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	### ### ##############################	8570         8580         8650         8640           ATABALAGARAGAAGGAGTGGCTCTTCTCTTTTCTCTTTTCTGAGTGACTTGAATCACAT		8720   8730   8740   8750   8760   8770   8780	### ### ##############################	8860 8870 8880 8890 8900 8910 8920 GAGTCAGAACTCTGGTGATTTCCCTCAATGAAGTGGAGTGATGCTCTCTCT	8940 8950 8960 8970
--	---	---	---	--	--	--	--	--	---	--	--	---------------------

	TTTTCATTCAACTGTGGTAGCCCCTTTTCATTCAACTGGTAGCTAGC	9940 9950 9950	10010 10020 10030 ACTGAAAGCAGACTGCTATAAGG	10090 AGGTAAGCATTTGTTTTATATTT 	10160 GTACACATTTCACTACCATT 	10230 AAGTCCTCATTTCTTTCGGTGT 	10300 TACATTTGAAAAATCAAAGACCT 	10370 10380 10390 10390 10390 10390 1011	10450 CGCTGAGGGTTTTCCTGAAGGT 	10530 10530	10590 10600 10 GCCATTGCTGAGCTGCCTGAACT 	10660 10670 1068 GTACAGCAGGTGATTGAGGACTG 
AGCCACCAAGTGGCTTAGAGGATGCCATGGGGGTTCCGGTGCACATTAAAAAA	9010  AAAATCTAACCAGGACATTCAGGAATTGCTAGGAAATCAGTCACCATGTTCAAAAGGTCTTTT	9080 9090 9100 9110 9120 9130 9140 TITITITICAGACTCTATIGCCCAGGCTGGAGTGCAATGGCATCATCTCGGCTCACTGTAACCTCTGCCT	9150 9160 9170 9180 9190 9200 9210 CCCAGGTTCAAGCGATTCTCCTGTCTCAGCCTCCCAAGTAGCTGGGATTACAGGCGTGCACCACCATGCCCG	9220 9230 9240 9250 9260 9270 9280 GCTAATTITIGIATITITIAGIAGACAGGGTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCTCCTGACC	9290 9340 9350 9360  TCGTCATCCCCCTGCCCTCCCCAAAGTGCTGAGATTACAGGTGTGAGCCACCCTGCCCAGCCGTCAAA	9370 9380 9430 9430 9430 9430 9410 9420 9430 9430 9430 9430 9430 9430 9430 943	9440 9450 9460 9470 9480 9490 9500 TGGTACAAGGATTCTGTCTTGAAGGGGAGGTGCTTCAGGATACCATATACAGCTCAGAAGTTTCTTTTAG	9510 9520 9530 9540 9550 9550 9570 GCATTAAATTTTAGCAAAGATATCTCATCTTCTTTTTTTT	9580 9590 9600 9610 9620 9630 9640 TGTAGAAAAAGTAAATGTGATTTAGGCTCATTGTAGAAAAGCTATAAAATGAATACAATTAAAGCTGTTAT IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	9650 9660 9770 9680 9720 TTAATTAGCCAGTGAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAAATGCA	9730 9740 9750 9760 9770 9780 9790 TATACTTTAATAATCATCTATTCTATACTCATCATTTTATTGAACTTCTTGTTCATCATCTTGTATA	9800 9810 9820 9830 9840 9850 9860 TACTTAATCGCTTTGCCATTTTGCAGACATTTATTTTGCTTCTTAATTTCTTTACATTTTGCTTACGGAATA

0 10040 10050 10060 10070 10080 10070 10080 10070 10080 10070 10080 10070 10080 10050 10050 10050 10060 10070 10080 | 10330 | 10340 | 10350 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10330 | 10330 | 10350 | 10350 | 10350 | 10350 | 10360 | 10350 | 10360 | 10350 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 10360 | 1036 10470 10480 10510 10200 10190 10180

730 740 750 760 770 780 790  TAAATAATCTCGTAGTTCCTCACTTCAGCTCAACCTGGGGGCTCCTTGAACCTGGAACTTCGGGTTTA	800   810   820   830   840   850   860   840   850   860   860   860   860   860   860   860   860   860   860   860   860   860   860   860   860   810   820   830   840   850   860	870   880   930	940 950 1000 1000 1000 1000 1000 1000 1000	1010   1020   1030   1040   1050   1060   1070   1080   GGTCTCTAGGGAGGCCTGGGGCCTTTCCCCCACTCTTGGCAATTGTTCTTTT	1090 1100 1150 1150 1150 1150 1150 1150	1160	1230 1290 1290 1290 CACTICTAAGTTATCACTAGGCATAGGGAGGTAGGGGAGTAATAATA CACTICTAAGTTACATTAGTTATTAGTTATTCACTAGGCATAGGGAGGTAGGGGAGTAATAATA CACTICTAAGTTACATTACATTAGATTATTCACTAGGCATAGGCATAGGAAGGTAGGAAGCTAATAATA 1230 1240 1250 1250	1300 1310 1360 1330 1340 1350 1360 CGTTTATTACTAGATTACTGGATTACAGATTACTAGATTATATACTCTTTTCAGGTTACAGATAAATAA	1370 1380 1390 1400 1410 1420 1430 1400 1700 1700 1700 1700 1700 1700 170	1450 1450 1510 TGTAGGACAGTGTTCTGTGGGTCACACGCCTCAGCACACACA
650   660   670   680   690   700   710   720   TCCCCGGGCTGTCCCCGAGCTGAGTGAGTTTTTGGAACCGCCCACTCCCCTTCCCCCAACTAGAATGCTTT	10   660   670   680   690   700   710   720	10	CCCCCGGCTGTCCCGGGTGTGTTTTTGGAACCGCCCATTCCCCCAACTAGAATGCTTTCCCCGGCTGTTCCCCCGACTGGAATGCTTTCCCCGGGTTGTTTGGAACCGCCCATTCCCCCCAACTGGAATGCTTTCCCCGGGTTGTTTTGGAACCGCCCATTCCCTTCCCCCAACTGGAATGCTTTGG	CCCCCGGCTGTCCCGGGTGTGTTTTTGGAACCGCCCATCCCCTACCCCAACTAGAATGCTTTCCCCGGCTGTCCCCGGCTGTCCCCGACTGGAATGCTTTCCCCGGGTGTCTCCCCGGCTGTCCCCGGCTGTCCCCGGCTGTCTCCCCGGGTGTTTTTGGAACCGCCCACTCCCTTCCCCCAACTGGAATGCTTTS0	TCCCCCGGCTGTCCCGGCTCTGCGGGTGACTTTTGGAACGCCCACTCCCCTTCCCCCAACTAGAAT	Troccogential	CCCCCGGCTGCCCGGCTCTGCGGAGTGGACTTTTGGAACCGCCCCACTCCCTCC		The control of the	1000   1000
	730 740 750 750 770 780 790 790 790 790 790 790 790 790 790 79	130   740   750   760   770   780   790	190	ATCRCATAGRACTCACCTCACCTCACCTCCTCACACCTCCACACTCCTTCACCTCCACACTCCCTTCACCTTCCACCTTCCACTTCCCTTCACCTTCCACCTTCCACTTCCTCC	TADATAAATCTCCTAGTTCCTCACTTGAGCTGAGCTGGGGCTCCTTGAACCTGGAACTCGG  TAAATAAATCTCCTAGTTCTCTCACTTGAGCTGAGC	TAMATAATCTCCTAGTTCCTCACTTGAGCTGAGCTGCGGCTCCTGAACCTGGAACTCCG  TAAATAAATCTCCTAGTTCCTCACTTGAGCTGAGC	THATAMATCTCTARGTTCCTCACTTCAGCTAGCTAGCCTGCGGCCTCTCAACCTGGAACTCCG TAAATAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTC	Taantaaatticcerasticcerasticcerasticcerasticcerestic	TABATRANTICCTRACTCCTCACTTCACCTCGGGGCCTCCTTGAACCTGGGAACTCGG   TABATRANTICCTCTCACTTCACCTCGGCTCCTGGGGCTCCTTGAACCTGGAACTCGG   TABATRANTICCTCTCACTTGACTTCACCTGGGGCTCCTTGAACCTGGAACTCGG   TABATRANTICCTCACTTGACTTGACTTGACTTGGGGCTCCTTGAACCTGGAACTCGG   S00	Tabathantictornation   Tabathantictornation

1450	2450 AGTCCP        AGTCCP		2600   1740   1750   1760   1770   1780   1790   1800   GCTCCAAGGAGACACAAGACACAAGACACAAGACACAAGACACAAGACACAAGACACAAGACATTAAGAAAACAAGAAAAAAAA		1980   1890   1900   1910   1920   1930   1940   2750	2810 CTGTAC               CTGTAC	1890   2030   2040   2050   2070   2080   1980	2120 2130 2140 2150 2160 GAAGGAGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA		2240   2250   2260   2270   2280   2290   2300   3100   3110   3100   3110   3100   3110   3100   3110   3100   3110   3100   3110   3100   3110   3100   3110	3170   3180
1450 1460 1470 1480 1500 1500 1500 1500 1530 1540 1550 ACATTTRACACAACAACAACAACAACAACAACAACAACAACAACAA	1590 1600 1610 1620 GCTTTGGTGGCAGAGCTCATGTCTCCACTTCATAGGTATGA	1660 1670 1680 1690 1 ATAATAAAATTTCATGTTGAGCAGAAATATTCATTGTTTAC 	1730	1810 1820 1830 1840 GATGACAATGACAAATGAGCAGAAAGATATACAACATCAG GATGACAATGACAAATGAGCAGAAAGATATACAACATCAG GATGACAATAGCAAATGAGCAGAAAGATATACAACATCAG 1810 1820 1830	1880 1890 1900 1910  TCAGGGCAAGTCACTCTGGGGCTGACACTTGAGCAGAGACA	1950 1990 1990 CAGTATTCCCAGGCAACTGAGTGGGCCTGGCAAGTTGGATTAAAAAGCGGGGGGGG	2020 2030 2040 2050 2 GTGTGTGTGTGGGGGGGGGGGGGGGGGGGGGAAA 	2090 2100 2110 2120 213 GCAGTATCCTGCTCCCTACTCACTAGGTGCTAGGAGCAC 	2170 2180 2190 2200  AAACTTTGCCACATGTCACTAGTAGACAAACTCCTGGTTA	2240 2250 2260 2270 GTGCTGGGGGGTAGGGGCCTAGGGGTAAGTGGGCTCAG [	2310 2320 2330 2340 CCTGTAGGCTGTGGTGAATTCTAGCCAAGGAGTAACGT 

2310 2320 2340 2350 2350 2370 2380 2440 2380 2430 2440 2420 2430 2440 2410 2420 2420 2430 2440 2410 2420 2430 2440 2440 2440 2440 2440 2440	2450 2510 2510 2520 AGTCCAGGGAAGAGGGAACAGGAACAGAAAGGGGAGAACAAACGGGAACACAAACGGGTGACAAACGGGTGACAAACGGGTGAGAAACGGGATGACAAACGGTGACAAACGAGAACAGAAAAGGGATGACAAACGATTGTCTCTTGAAAGGCAGGC	2530 2590 2590 2590 2590 2590 2590 2590 259	2600   2610   2620   2630   2640   2650   2660	2670 2680 2690 2710 2720 2730  AGCAAAACCCCTTCTCTACAAAAATAGCTGGGTGTGGTGGCATGCCCCTGTGATCCTAGCTA	2740 2750 2800 2800 CTCGGGAGGTGAGGTGAGGGTATTGCTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCCATGACTGCCA CTGGCCA CTGGCTGAGGCTGAGGTGAGCCTATGCTTGGTTGAGCCCAGGAAGTTGAGGCTGCAGTGAGCTTGAGCCAGGAGGTTGAGCCAGGAGGTTGAGCTGAGCATGATTGAT	2810 2820 2830 2840 2850 2860 2870 2880 CTGTACTTCACCTAGGGAGAGACCAGACCCTGCTCCCCTGAAAAAGAGAGAG	2890 2940 2950 2950 2930 2940 2950 2950 2940 2950 2940 2950 2940 2950 2940 2950 2940 2950 2950 2950 2950 2950 2950 2950 295	. 2960 2970 2980 3900 3000 3010 3020  GAAGGAGARAAAAGACAGTITGGGGTAAATCAAGAICTGGAITTTGGAACATGTITAAGITTTGAAATTCCA	3030 3090 3090 3050 3050 3090 3090 3090	3100 3150 3160 3160 3160 3160 3160 3160 3160 316	3170 3180 3230 3240 GCTTGGCCAACATGGTGAAACCCCATGTCTACTAAAATACAAAATTAGCCTGGTGTGGTGGCGCACGCCT 
---	--	---	--	---	---	--	---	--	---	--	---

3250 3260 3310  ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAGATCCCTTGAACCCAGGGGGTGCAGGTTGCAGTGAGCT  ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAATCCCTTGAACCCAGGAGGTGCAGGTTGCAGTGAGCT  ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGGAATCCCTTGAACCCAGGAGGTGCAGGTTGCAGTTGAGTGAG	AAAAAAACTGAAGGAATTATTCCCCCGGACTCAATTTGCCCTGAGCACCCTGAGTTCAAC 3390 3400 3410 3420 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510 3520 3520 3500 3520 3500 3500 3500 350	3610   3620   3630   3640   3650   3660   3670   3650   3650   3650   3670   3650   3700   3710   3720   3730   3740   3740   3740   3750	3750   3760   3770   3780   3790   3810	90   3900   3910   3920   3930   3950   4050   40	4040 4050 4060 4070 4080 4090 4100  GAGAGGGGCCTCACTTCCTGAGGGTTGTCACTTTTCATGCATCTTGAAGGAAACAGCTGG
3250 ATAGTCCCAGGTTTTCAGAGGGCTTAGGTAGGAGAAAACTGCCAGGTTTTCAGAGGGCTTAGGTAGG	AAAAAAACTGAAGGAATTATTCCTCAGGATTTGGG 3390 3400 3410 3420 3460 3470 3480 3490 TACCATGGCTAGACACCTTAACATTTTCTAGAAT 1	3610 3620 3630  ACCCAGGACTGTCAITATGGAAGAAGACAGGACTGC	3750 3750 3760 3770 3770 3770 3770 3770 3850 3850 3850 3850 3850 3850 3850 385	3910 3920 3606 3910 3920 3606 3920 3606 3920 3970 3980 3980 3970 3980 3970 3980 3970 3980 3970 3980 3970 3980 3970 3980	4040 4050 4060 40 GAGAGGGGCCTCACTTCCTGAGGTTGTCAGAGCT 

GGGGAT        GGGGAT	ACCCTG        ACCCTG	4320 GATGGG        GATGGG	4390 ACCAAG        ACCAAG 4390	60 GCACAG        GCACAG 60	TGCCCC 	GCTGAG        GCTGAG	4680 GATGTA        GATGTA 4680	4750 ATGGCC [      ATGGCC 4750	20 GCCGGG        GCCGGG	GTTTGA        GTTTGA	TGCGCA        TGCGCA	5040
4170 TTGGTCCTTG           TTGGTCCTTG	4240 GAGTCCCAC          GAGTCCCAC 4240	4310 TACGGGTAT         TACGGGTAT 4310	380 GCCTGGCCC H       GCCTGGCCC 380	GACTGCCTV GACTGCCCTV GACTGCCCTV	4530 ACACACTTC          ACACACTTC 4530	4600 TCAGAGGTG           TCAGAGGTG	4670 TATAATTGA          TATAATTGA 4670	740 GAAGIGICI          GAAGIGICI 740	0 48 AATGTCAAG          AATGTCAAG	4890 AGGTCAGGA         AGGTCAGGA	4960 TCACAGTCA          TCACAGTCA 4960	5030
4110 4120 4130 4140 4150 4160 AAGTCTGAGGTCTTGTGGGAGGGAAAGGAATTTGCTTCCTGAGATCATTTTTTTT	4180 4190 4240 GGTGGAAATAGGGACCTATTCCTTTGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTCCCACAC	4260 4270 4280 4290 4300 4310 4320 CATCCTGGGCTTACTAGAAGTACCAGAGAGACTACCGAGGGCTACTGGAAGTACGGGTATGATGGGCTACTGGGAAGTACGGGGTATGATGGGCTACTGGAAGTACGGGTATGATGGGCCTACTGGAGTAGAGAGAAGACAACAGAGAAAGACAAACAA	4330 4340 4350 4360 4370 4380 4370 4380 CAGGACCACCACCACCACCACCACCACCACCACCACCACC	4400         4410         4420         4430         4440         4450         4460           CTGGAGTGGGAAAGGCTACTACTGGAGGGCTGCTTGCTGGAGGGACTGCCTTGCAGGCTACTGGAGAGGACTGCTGGAAGAGGAAGAGGAATTCGGGCCAGGCAGAGAGGCCTACTTGGAGAGAGA	4470         4480         450         4510         4530           CTGCAGCAGTTGCTGGAGAGAGAGAGAGAGAGATATGGTGGAAACACTTCTGCCCC         [1] [1] [1] [1] [1] [1] [1] [1] [1] [1]	4550 4560 4570 4580 4570 CTAGTGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	10   4620   4630   4640   4650   4660   4670   4680   4620   46	4690 4700 4710 4720 4730 4740 4750 GAGACAGCCACAAGGGATTAATTTCTTTTCTCCATGCATAGGCTCAAAGGGAAGTGTCTATGG [	4760 4810 4820 CTTGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT	4830 CACGGGGCCACCCTGTAATCCCAGCACTTTTGGAGGCCGGGGGGGG	0 4910 4920 4930 4940 4950 CAGCCTGACAAAATTACAAAAATTAGCTGGTCACAGTCATGCGCACACTGACGCAAATACAAAAATTAGCTGGTCACAGTCATGCGCACACGCACAGTCATGCGCACAACTGCGCACATGCTGCCTGACCAACATGCTGACAAAATTAGCTGGTCATGCGGCAAGCGCGCAAGAGCCGCAAGAAAATACAAAATTAGCTGGTCATGCGGCAAGAGCGCGCAAGAGCGCGCAAGAGCAGATGAAAAAAAA	5020
4150 ATTTGCTTCC           ATTTGCTTCC	4220 NAGGCTGGGG NAGGCTGGGG 4220	1290 FACCGAGGG            FACCGAGGG	50 43 BAGAGCAGC                 BAGAGCAGCA	4440 DAGGGCCTAC	4510 SCAACAAGG           SCAACAAGGI 4510	4580 3GAATCCCTC           3GAATCCCTC	1650 VATCCTAGAG            VATCCTAGAG	20 47 CATGCATATO	480C PACCTGTTAA           PACCTGTTAA	4870 3CCGAGGCGC           3CCGAGGCGC	4940 AATACAAA           AAATACAAA	5010
4140 AGGGAAGGA          AGGGAAGGA 4140	4210 3CAGTTAAC           3CAGTTAAC 4210	280 AGACAACAGT           AGACAACAGT	0 ACTGGATTGG          ACTGGATTGG	4430 CAGGCAGAA(           CAGGCAGAA( 4430	4500 IGTTTTGGA(           IGTTTTGGA( 4500	4570 3CAGGGCACC            3CAGGGCACC 4570	640 SACTITCIC SACTITCIC SACTITCIC	0 TCTTTTCTCC           ICTTTTCTCCC	4790 STATATTTA:          STATATTTA: 4790	4860 CTTTGGGAGG           CTTTGGGAGG	4930 ICTCTAAAA           ICTCTAAAA 4930	000
4130 SCAGGGAAG SCAGGGAAG 4130	4200 CCTTTGGTT(          CCTTTGGTT	70 4.7 AATGCAAGA.AATGCAAGA.AATGCAAGA.	435/ CCCTGACAC/          CCCTGACAC/ 435/	4420 3ATTCGGGC          3ATTCGGGC	4490 3GGGAGAGG          3GGGAGAGG 4490	1560 SAGGAGGTT          SAGGAGGTT 1560	30 40 CTGGGAAGG [        CTGGGAAGG	471 3GTTTAATT         3GTTTAATT	4780 IAATCTTTTV          FAATCTTTTV 4780	4850 ATCCCAGCA          ATCCCAGCA 4850	4920 IGAAACCCG          IGAAACCCG	90
4120 FTGTGGGA(          FTGTGGGA(	90 SACCTATT         SACCTATT	42' 36CTGTGA 1               36CTGTGA 42'	4340 SAATTCTG(         SAATTCTG( 4340	4410 AGGCACAA(         AGGCACAA( 4410	4480 CTGGAGCT(         CTGGAGCT( 4480	50 SCAGAGTGG         SCAGAGTGG	46: ICCAAATT ICCAAATT	4700 AAGTCATG(         AAGTCATG 4700	4770 TTAACCAA'          TTAACCAA' 4770	4840 CCCCTGTA         CCCCTGTA 4840	10 CAACATGG'         CAACATGG'	49
10 CTGAGGTC CTGAGGTC CTGAGGTC	413 GAAATAGG         GAAATAGG	4260 TCATCCTG         TCATCCTG	4330 ACCACCTT(         ACCACCTT( 4330	4400 AGTGGGAA          AGTGGGAA 4400	70 AGCAGTTG(         AGCAGTTG( 70	45: CTCTAGTGG         CTCTAGTG	4620 TGTGCCTC TGTGCCTC 4620	4690 ACAGCCAC         ACAGCCAC 4690	4760 CTTTTTAT          CTTTTTAT 4760	30 GTGGCTCA( GTGGCTCA( GTGGCTCA( 310	49: AGCCTGACO         AGCCTGACO	4980
41 AAGT AAGT 411	4180 GGTG GGTG 4180	4250 CAGGTC       CAGGTC	CAGG CAGG	CTGG	CTGC CTGC CTGC A44	4540 TATACTC         TATACTC 4540	4610 GCTG      GCTG 4610	TGAG 	CTTG      CTTG	48 CACG	4900 GACC GACC 4900	4970

CCTGIAGICCCAGCTAATTGGAAGCTGAGGCAGGAGCATCGCTTGAACCTGGAAAGCGGAAGTTGCACTGA 	S050   S060   S070   S080   S090   S100   GCCAACATCGGGCCCCACTCTCGGGCCTAGGCCTAGGCGGGGGGGG	5120 5130 5180  AAAAGAGANTTCAGAGATCTCAGGATCAATAACAACAGAAAATATCAAGTGAGGCCACTTATCAG	5190 5200 5210 5220 5230 5240 5250 AGTAGAAGAATCCTTAGGTTAAAAGTTTCTTTCATAGAACATAGCAATAATCACTGAAGCTACCTATCTTA	5260   5270   5280   5290   5300   5310   5320   CAAGTCCGCTTCTTATAACAATGCCTCCTAGGTTGACCCAGGTGAAACTGACCATCTGTATTCAATCATTTT	5330         5340         5350         5360         5370         5380         5400           CAATGCACATATATATCTATCAGAACAAGAACATGGGTAACAGATATGTATATATA	5410   5420   5430   5440   5450   5460	5480   5490   5500   5510   5520   5540     6700000000000000000000000000000000	5550   5560   5570   5580   5590   5600   5610   CCAGTCTTCCTGCAAGGGTAAAGACACCCTCTCCTTCCTT	5620   5630   5640   5650   5660   5670   5680   GRANGGTGACACTCTTCACTGACCACTGTCGGGCCTTGAACTACCCCCAGGGGGGTGTTCGGGCCTTGAACTACCCCCAGGGGGGTGTTCGGGCCTTTGAACTTACCCCCAGGGGGGTGTTCGACCACTTTCACGTCGTTCGACCACTTTGACTTACCGTGTTACGGCGTTTGAACTTACCCCCAGGGGGGGG	5690         5700         5710         5720         5760           AACATCACCATGAACTACATGCCAAGGACTTCGAACCTAATG           HIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	5770         5780         5830           CCCAATGGGGATGCTACCAGGATAACCTTGGCTGTACCCCCTGGGGAAGACAGAGATATACG	5840 5850 5860 5870 5880 5890 5900 TGCCAGGTGGAGCACCCTGGATCAGGTCTGGGGTATGTGACGAGGCCAGG

5980         6000         6010         6020         6030         6040           TETTGTTTGTTTTTGTTTTTGTTTTTGTGCCTCAC           TETTGTTTGTTTTGTTTTTGTTTTTGTTTTTGTTTTTGTTTT
6050   6060   6070   6080   6090   6100   6120
6130 6140 6150 6160 6170 6180 6190 TGTTCKTRATATAGGAAGGGGTTCAAGTGAGTAGGAACAGGGGAAGTCTCTTAGTACCTCTGC
6200   6210   6220   6230   6240   6250   6260   6260   6260   6260   6260   6260   6260   6260   6260   6260   6260   6260   6200   6220
6270 6280 6290 6300 6310 6320 6330 TTGGGGACACCACACTCCTCCCGAGAAATAATGGTTCTCCCCAGAATGAAAGTCTCTAATTCAAC
6340 6350 6360 6370 6380 6390 6400  AAACATCTTCAGAGCACCTACTATTTGCAAGAGCTGTTTAAGGTACTACAGGGGCTTTGAGGTTGAGAAGT
6410 6420 6430 6440 6480 6480 6480 6480 6480 6480 648
6560 6570 6580 6590 6600 6610 6620 TGGGGATCAAGATAGCCTTCTGCALCTTGAAGAAGCTGGATTCCALTAGCTGAGGTTGAAGATGATGGG
6630 6640 6650 6660 6670 6680 6690  AGTCTACACACACCACACCACACACACACACACATACACACATACTGCGACATTACAAATAATTACATACA
6700 6710 6720 6730 6740 6750 6760 TGTACCTTAACCCTGAGTTTGCGTAAGCTATCACCACCAATTATGCATTTCTACCCCCTGAACATCTGTGGT 

Title	### ##################################
### CTATA CCCTCTA ACCTCTA CCTA CCTATA CCCCATA ACCTCTA ACCTCTA ACCTCTA ACCTCTA ACCTCA A	7420 7430 7440 7450 7460 7470 7480  7490 7500 7510 7520 7530 7550 7560  AAATTTGGGGGACTTACATGATTCATTTAACATCTGAGAAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT  AAATTTGGGGGACTTACATGATTCATTTTAACATCTGAGAAAAGCTTTGAACCCTGGGACGTGGCTAGTCAT  7490 7500 7510 7520 7520 7530 7550  7570 7580 7590 7600 7610 7620 7630  AACCTTACCAGATTTTTACACATGTATCTAGGATTTTCTGGACCCGTTCAACTTTTCCTTTGAATCCTCTC

### ### ##############################	### ### ### ### ######################	### ### ##############################	### 8950 ### 8950 ### 8950 ### 8950 ### 8950 ### 8950 #### 8950 #### 8950 #### 8950 #### 8950 #### 8950 ####################################	9080   9090   9100   9110   9120   9130   9140   917TTTTTTTTTTTTTTTTTTTTGAGACTGGCTGGCAATGGCAATGGCAATGGCAATGGCAATGGCAATGACTCTTGGCTTGCTT		9290 9300 9310 9320 9330 9340 9350 9360 TCGTGATCTGCCTGCCTGCCTGCCTGCCTGCCTGCCTGCTGAAA TTGCTGTGATGGCTGGCTGCTGAAA TCGTGTGATGCTGCTGCCTGCCTGCCTGCCTGCTGAAA TCGTGTGATGCTGCTGCCTGCCTGCCTGAAA TCGTGATGCTGCCTGCCTGCCTGAAA TGGTGATTACAGGTGTGAACCTCTGCCTGAAA 9320 9330 9330 9330
--	--	--	--	--	--	---

9370 9380 9400 9410 9420 9430 AGAGICITAAIAITAITAITAITAICCAGAIGGCAGCAIGAATG	9510 9520 9530 9540 9550 9550  GATTAARTTTAGCAAGATATCTCATCTTCTTTAAACCATTTTCTTTTTTGGGTTAGAAAGTTA	9580 9590 9640 TGTAGAAAAAGTAAATGTGATTAAGGCTCATTGTAGAAAGGCTATAAAATGAATACAATTAAAGCTGTTAT	9650 9660 9670 9680 9710 9720 TTAATTAGCCAGTGAAAAACTATTAACAACTTGTCTATTACCTGTTAGTATTATTGTTGCATTAAAATTGCA TTAATTAGCCAGTGAAAAACTATTAACAACTTGTTGTTACTTGCATTAAAAATGCA TTAATTAGCCAGTGAAAACTATTAACAACTTGTTATTACCTGTTAGTATTATTGTTGCATTAAAATGCA 9650 9660 9670 9680 9730	9730 9740 9750 9750 9760 9770 9780 9790  TATACTTAATAATGTATTCTATTGTATACTGCATGATTTTATTGAAGTTCTTGTGTGTATA  [	9800 9810 9850 9830 9840 9860 TACTTAATCGCTTTGTCATTTTTGGAGACATTTATTTTGCTTCTAATTTCTTTACATTTTGTCTTACGGAATA	9870 9880 9890 9900 9910 9920 9930 TITICATICATICACCCAATIDATICGTOTITICTICACCCTAGGGACATIGCGTOTIAGGTIGTAGG	9940 9950 9960 9970 9980 9990 10000 ACATTGGTTATTTACCAGCAAACCATTGGAAAGCATATGACAATTATTTCTCTCTTAATATCTTACTAT	10010	10090 10100 10110 10120 10130 10140 10150	10160 10170 10180 10190 10200 10210 10220 GTAACACATTTCACTAACATTTACTAAACATCAGCAACTGTGGCCTGTTAATTTTTTAATAGAAATTTT	10230 10240 10250 10260 10270 10280 10290
		9520 9530 9530 9570 TITACCAAACATATCTCATCTTTTAAACCATTTCTTTTTTTGGGTTAGAAAA	9520 9530 9540 9550 9560 957  TITAGCAAAATATCTCATCTTCTTTTAAACCATTTTTTTTTT	9510   9520   9530   9540   9550   9560   9550	9510   9520   9530   9540   9550   9560   9560   9560   9550   9560   9550   9550   9550   9550   9550   9550   9550   9550   9520	S510   S520   S550   S560   S660   S660	SECONTITUTION   SECONTITUTION	9510 9520 9550 9560 GCATTANATTTTAGCAAAGATATCTCATCTTTTAAACCATTTTTTTT	SE20   SE20   SE30   SE30	9510 95210 95310 95310 95310 95310 95310 95310 95310 95310 95310 95310 9	9510 0CATTANATTTTTGCAAAGATATCTCTTTTTTTTTAAACATTACTTTTTTTT

ATAAATTCTTAAGGTCAAC  STAAATTCTTAAGGTCAAC  280 10290  ACCATTCAAACCATGG  ACCATTCACAACCATGG  AACCATTCACAAACCATGG	10430 10430 	10570 10580  TGAATTGCTGGAATCACAG  TGAATTGCTGGAATCACAG  10570 10580  TGATAATCATTGAGTAATCACAG  TGATAATCATTGAGTCAA  TGATAATCATTGAGTCAA  TGATAATCATTGAGTCAA  TGATAATCATTGAGTCAA  TGATAATCATTGAGTCAA	0 10720 3TATTATAATAATGTCATC 	10790 10800  AAAAACAAAACTCTCTC		Significance = 7.99 Mismatches = 2 0	60 ATATTTAAATATCTAAAGT                  ATATTTAAATATCTAAAGT 60	130 ATTTAAAAACCAAGGGGA                   111aaaaaCCAAGGGGA 130
AAGTCCTCATTTTCTTTCGGTGTTTTTTAAGCTTAATTTTTCTGGCTTTATTCATAAATTCTTAAGGTCAAC	10370   10380   10390   10400   10410   10420   10430   10440     TAGTAAAGAGAAGGTCACCACGTGGCCCATAGGTAATGTACCGGTGGCCGGTGGCCGGTGGCGGGTGGTGGCGGTGGTGG	10520   10530   10540   10550   10560   10570   10580	10660   10670   10680   10690   10700   10710   10720   GTACAGCAGGTGATTATATAATAATGTCATGTGAGGTACAGGCCAAAATTCTTATGTTGTATATAATAATGTCATGTGAGGTACAGGCCAAAATTCTTATGTTGTATATAATAATGTCATGTGAGGTGATGTTGATGTGATGTGAGGGTGATGGTGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATAATGATCATGTCATGTGTGTG	10730 10740 10750 10760 10770 10780 10790 10800 TTATAATACTGTCAGTATTTATAAAAATTCTTCACAAACTCACACACA	10810 X TAAAATCCCCAAATTTTCATAAAC	4. US-09-497-957-1 (1-10825) US-09-497-957-7 Sequence 7, Application US/09497957 Initial Score = 10823 Optimized Score = 10823 S Residue Identity = 99% Matches = 10823 Macches = 10823 Matches = 10823 Matche	x 10 20 30 30 40 ECTAAGGTTGAGATTTTGAAAATCATAAATATTTAAATATTTAAAGTTTTAAAGTTTTAAAGTTTTAAAGTTTTAAAGTTTTAAAGTTTTTAAAGTTTTTAAAGTTTTTAAAGTTTTTT	80 100 110 120 130 140 TCAGATCAGAACATTGCGAAGCTACTTTCCCCAATCAACAACACCCCTTCAGGATTTAAAAACCAAGGGGGA

Carter   C	GCGCGCAAAGACGTTGGGGAILTGAATTLTTCALCALLCCCCCCCCCCCCCCCCCCCCCCC	GGCGCGAAAGAGTGGGGGATCTGAATTCTTCACCATTCCACCTTTGGTGACCTGGGGGTGGA 940 950 1000	0 1020 1030 1040 1050 1060 1070 1080
150   150		GGCGCGA 940	1010

	CAGTATTTCCCAGGCAAACTGAGTGGGCCTT 1950 1970 1970 2020 2030 2040 GTGTGTGTGTGGGGGGGGGGGGGGGGGGGGGGGGGG	2090 2100 2110 2100 6GAGTATCTGTCTCCCTTAGGTGGGTAGGTGGGTAGGTGGGTAGGTGGTCTCCCTACTCACTAGGT 2090 2100 2190	AAACTTTGCCACATGTCACCTAGTAGACAA 	GTGCTGGGGGTAGAGGCCAAGAAGTAGGTA 	100 120 120 120 120 120 120 130 100 100 100 100 100 100 100 100 10	2380 2400 GGCTGCTATGGAAAGCAGAATGAAGGA [	2450 2460 2470 24 AGTCCAGGCAAGGTAGTGGAGTGGGGTG 	2530 2540 2550 TATATICTGAAGGAAGTTGCTGAAGGATTC	2600 2610 2620 GCTCATGCCAAGAGGGGCCAAGGAGACC	2680 2690 AGCAAAACCCTTCTCTCTAAAAATACTACAAAAAAAAAA	2740 2750 2760 CTCGGGAGGCTGAGGTGGAGGTAITGCTT
GGTCTCTAGGGTGGGAGGCTCTGAGAGAGGCCTACCTCGGGGCCTTTCCCCCACTCTTGGCAATTGTTCTTTT .		1230 1240 1250 1260 1270 1280 1290 CACTTCTAAGTTACATATCTGATCTTATTTGATTTTCACTAGGGAGGTAGGGAGGTAGGAGGTAATAATA	1300	1370	1450	1520   1530   1540   1550   1560   1570   1580   1570   1580   1570   1580   1570   1580   1570   1580   1570   1580   1570	1590 1600 1610 1620 1630 1640 1650 GCTITGGTGGCGAGAGCTCATGATAGCTATGATTCTTAAACATCACACTGCATTAGAGGTTGA	1660 1670 1680 1690 1700 1720 ATAATAAATTICATGTTGAGCAGAAATATTCATTGTTTACAAGTGTAAATGAGTCCCAGCCATGTTGCA	1730	1810 1820 1830 1840 1850 1850 1870 GATGACAATAAGCAAAAGGATATACAACATCAGGAAAATCATGGGTGTTGTGAGAAGCAGAAAGGAAGG	1880 1990 1910 1920 1930 1940 TCAGGGCAAGTCACTGGGGGCTGACACTTGAGGAAATAAGAATGATATTGACTGGGAG

360 GATGCTATGAG H	3750 TGTTGCTCTGT            TGTTGCTCTGT 3750	3820 TTCCTTGTTTG            TTCCTTGTTTG 3820 38	3900 GGAGCCCGAAC 	AGGGTGGATO AGGGTGGGATC AGGGTGGGATC	4040 GAGAGGGGGCC GAGAGGGGGCCC GAGAGGGGCCC GAGAGGGGCCC	4110 AAGTCTGAGGTC           AAGTCTGAGGTC 4110	4180 GGTGGAAATAGG 	4260 4260 CAGGTCATCCTV 	CAGGACCACCT	4400	4470 CTGCAGCAGTT
2740 2750 2760 2760 2770 2780 2800 2800 2810 2820 2820 2830 2810 2820 2830 2840 2820 2830 2830 2830 2830 2830 2830 283	2890 2950 2950 2950 2950 2930 2940 2950 1 2940 2950 1 2950 2950 2950 2950 2950 2950 2950 2950	2960 2970 2980 3000 3010 3020 GAAGGCAGAGAAAAGAGCTTTGGGCTAAATCAAGGATCTGCATTTGGGACATGTTTAAGTTTGAGATTCCA	3030 3040 3050 3060 3070 3080 3090 GTCAGGCTTCCAAGTGAGGCCCACATAGGCAGTTCAGGACCCAAGGCTGGGGCACCGTG	3100 3110 3120 3130 3140 3150 3160 GCTCACTTCTGTAATCCTGGGCCAAAGCTCAGGTCAGGGTCAGGAGTTTGAGACAAAGCTCAGTCAG	3170 3180 3190 3200 3210 3220 3220 3230 3240 3210GCTTGGCCAACATGTGAAAACCCCATGTACAAAAATTAGCCTGGTGTGGTGGTGGCGCCACGCCT [	3250 3260 3270 3280 3290 3300 3310 ATAGTCCCAGGTTTTCAGGAGGCTTAGGTAGAATCCCTTGAACCCAGGAGGTGCAGGTTGCAGTGAGCT	3320 3330 3340 3350 3360 3370 3380 GAGATTGTGCCACTGCACTGGTGATAGAGTGACTCTGTCTCAAAAAAAA	3390 3400 3410 3420 3430 3440 3450 AAAAAAAAAACTGAAGGTTTTCCCTGAGTCTAATTTGCCCTGAGCACCAACTCCTGAGTTCAAC	3460 3470 3480 3490 3500 3510 3520 TACCATGGCTAGACACCCTTAACATTTCTAGAATCCACCAGCTTTAGTGGAGTCTGTCT	3530 3540 3550 3560 3570 3580 3590 3600 TTGGAATAGGATCTGGGGGTGGCGGCCACGTCTGGCAGAAAAGCACACACA	)

3610 3620 3630 3640 3650 3660 3670	3750 3760 3770 3780 3790 3800 3810 TGTTGCTCTGCAGGTTCACACTCTTGCACTACCTCTTCATGGGTGCCTCAGAGCAGGACCTTGGTCT	3820 3880 TTCCTTGTTTGAAGCTTTGGGTGATGACCAGCTGTTCGTGTTCTATGATCATGAGAGTCGCCGTGT TTCCTTGTTTTGAAGCTTTGGGCTACGTGGATGACGCTGTTTTGTTTTATGATGATGGCCGTGT TTCCTTGTTTGAAGCTTTGGACTTATGACGTTACACGTGTTCGTGTTCTATGATGATGATGGCCGTGT 3820 3830 3840	3890 3900 3910 3920 3930 3940 3950 3960 3960 3960 3960 3960 3960 3960 396	3970 3980 3990 4000 4010 4020 4030 AGGGAGCACCARGITCACTGITTCACACTATIATGGAAAATCACACACACACACATGTG	4040   4050   4060   4070   4080   4090   4100   4040	4110 4120 4170  AAGTCTGAGGTCTTGTGGGGGCAGGGAAGGAAGTTTGCTTCCTGAGATCATTTGGTCCTTGGGGAT	4180 4240 GGTGGAAATAGGGACCTATTCCTTTGGTTGAGTTAACAAGGCTGGGGATTTTTCCAGAGTTCCACCCTG GGTGGAAATAGGGACCTATTCCTTTTGGTTGCAGTTAACAAGGCTGGGGATTTTTCCAGAGTTCCACCCTG GGTGGAAATAGGGACCTATTCCTTTGGTTGGAGTTAACAAGGTTGGGGATTTTTCCAGATCCCTGAGTTACAAGGGTTGGAGTTAACAAGGTTAACAAGGTTAACAAGGTTAACAAGAGTTAACAAAGATTATTCCAGATCCCTGAACCTGTAACAAGGTTAACAAAGGTTAACAAAGATTTTTCCAGAACTCCCACACCCTGAACAGTTAACAAAGATTAACAAAAAGATTAACAAAAAAAA	4250 4260 4310 4320 4320 4320 4320 4320 4320 4320 432	4330 4340 4350 4350 4350 CAGGACCAGAGACCCAGGGCCTGGCCACCAAG  CAGGACCACCTTGAATTCTGCCCTGACACTGGATTGGAGAGCAGGAGAACCCAGGGCCTGGCCCACCAAG  [	4400 4410 4420 4430 4440 4450 4460 CTGGAGTGGGAAAGGCACAGGCAGGCAGGAACAGGGCCTTACCTGGAGGGACTGCCCTGCACAG	4470 4530 CTGCAGCAGTTGCTGGAGAGAGGTGTTTTGGACCAACAAGGTATGGTGGAAACACACTTCTGCCCC
		3760 3770 3780 3790 3810  TILLIA	AGGTTCACACTCTTGCACTACCTCTTCATGGGTGCCTCAGAGCAGCCTTGGAGTCACACACCTTGCAGAGCTTGCAGAGCTTGCAGAGCAGAGCAGAGCTTGCAGAGCAGAGCAGAGCAGAGCAGAGAGAG	3750 3760 3770 378  TGTTGCTCTGTCTCCAGGTTCACACTCTTGCACT	3750 3760 3800 3700 3780 3790 3800 3800 3750 3750 3800 3750 3750 3800 3750 3800 3800 3750 3800 3800 3800 3800 3800 3800 3800 38	3750 3760 3800 3700 3780 3790 3800 3800 3750 3750 3800 3800 3800 3800 3800 3800 3800 38	3750   3760   370   3780   3890   3890   3750   3750   3750   3800   3750   3750   3750   3750   3800   3750   3750   3750   3750   3750   3800   3900   4000   4000   4020   4	3750   3760   3760   3770   3780   3780   3880	1750   3760   3770   3780   3790   3790   3750   3860	3750   3760   3770   3780   3890   4000   4010   4020   4020   4020   4030	3750   3760   3770   3780   3790   3890   3990   4000   4010   4010   4020   4030

1510	
------	--

5410   5420   5430   5440   5450   5470   5460   5470   5460   5470   5460   5470   5470   5470   5470   5470   5470   5470   5470   5470   5470   5470   5470   5470   5450	5480 5490 5500 5510 5520 5530 5540 GTCTCCCTGTAGCTTGTTTTCTGAAAAGGCTATTTCCTTCC	S550   S560   S570   S580   S590   S600   S610   CAGTCTTCCTGCAAGGGTAACAGATCCCTCTTCCTTTCCTGTCTTCTGTCAAGGCGTCCTTTG   CAGTCTTCCTGGCAAGGGTAAACAGATCCCTCTCTCTTTCTT	5620   5630   5640   5650   5660   5670   5680   6700   5680   6700   5680   6700	S690   S700   S710   S720   S730   S740   S750   S760   S760	S770   S780   S780   S830   S830   S830   CCCAATGGGGAAGACTACCATGGGTAACCTTGGCTGTGCTGTGCGGAAGAGAGAG	\$840	5910         5920         5930         5940         5950         5970           AGTIGAGAAAATCTATTGGGGGTTGAGGAGTGCCTGAGGAGTAATTATGGCAGTGAGATCTGC	5980         6000         6010         6020         6030         6040           TCTTTGTTAGGGCTTTTACTTTTTCTGTTTTTAGAGCCCTCAC           IIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	6050 6060 6070 6080 6090 6100 6110 6120 CGTCTGGCACCCTAGTCATTGAGTCATCATGTGAATTT	6130 6140 6150 6150 6150 6190 6190 6190 6190 6190 6190 6190 619	6200 6210 6220 6230 6240 6250 6260 CCCAGGGCACCAGGGAAGCATTTTCTCATTTATATTCTCTTTTTTTT	6270 6280 6290 6300 6310 6320 6330
---	--	---	---	---	---	-------	---	---	--	---	--	------------------------------------

	7350 7360 7310 7380 7390 7410  CGGTGATCCCTAGGCTGTCCCCCCCCCCCCCCAAACTCCCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCAAGCTCCCTCC	7490   7500   7510   7520   7530   7540   7550   7560     AAATITGGGGGACTTACATITTAACATCTGGGAAAAGCTTTGAACCCTGGGGCGAGCTGATCAT	T640   T650   T660   T670   T680   T690   T700	7780 7790 7800 7810 7820 7830 7840  GGTAGTTATTAGCAGGAAATATCTTGAAAGGGGTTGTGAAGAGGTTTTTTTC	)
	6410 6420 6430 6440 6450 6460 6470 6480  6490 6500 6510 6520 6530 6540 6550  ACCCCATGAGGTCCTAAAGCAGGAAGCAAATGCTTAGGGTGTCAAAGGAAAGAATGATCAGTTCAGC	6550   6570   6580   6630	6700 6710 6720 6730 6740 6750 6760 6770 6780 6780 6810 6820 6830 GTAGGGAAAAGAGAATCAGAAAGAAGACCAGCTCATACAGACTTTTGGGATATTGGGTTATGA [	6850 6860 6870 6880 6890 6900 6910  6920 6930 6940 6950 6960 6970 6980  AGAAGTTAGATGAGGAGACCAGTTAGAAGCCAATAAGCATTTCCAGATGAGATATCTTCTTCTTTCT	100

ATGATAAAAGCACTTTCGTGTCCCGACTCTTCTGAGCACCTTACTTA	8860 8870
8070         8100         8130           ACANTAGTCTATGAGATAGGTACTATTATCTTTTTTAAATGAAGAAGTGAAGTAGGGCGGGC	AGCCACCAAGTGGCTTAGA 
8150   8160   8170   8180   8190   82 	9010 AAAATCTAACCAGGACATT
8210   8220   8230   8240   8250   8260   8270   8280	9080 TTTTTTTTGAGACTCTA 
	9150 CCCAGGTTCAAGCGATTCT                CCCAGGTTCAAGCGATTCT
###   ####   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ###   ####   ####   ####   ####   ####   ######	9220 9220 GCTAATTTTGAATTTTTA 
8430   8440   8450   8460   8470   8480   8490   8490   8490   8490   8490   8490   8490   8490   8490   8490   8490   8490   8490   8490   8490   8480	9290 TCGTCATCCGCCTGCCTCG TCGTCATCCGCCTGCTCG TCGTCATCCGCCTGCCTCG 9290
## ## ## ## ## ## ## ## ## ## ## ## ##	9370 AGAGTCTTAATATATATAT 
STO   8580   8590   8600   8610   8620   8630   8640	9440 9450 TGGTACAAGCATTCTGTCT'                  TGGTACAAGCATTCTCTCTCTCTCTCTCTCTCTCTCTCTC
10   10   10   10   10   10   10   10	9510 GCATTAAAITTTAGCAAAG 
### ### ##############################	9580 TGTAGAAAAAGTAAATGT 
### ### ##############################	SO AGTGAA AGTGAA SO
8860 8910 8920 GAGTCAGAACTCTGGTGGTATTTCCCTCAATGAAGTGGAGTAAGCTCTCTCATTTTGAGATGGTATAATGGA 	9730 TATACTTTAATAAATGTAT 

B860   B870   B870
---

9800 9810 9820 9830 9840 9850 9860  TACTTAATCGCTTTGTCATTTTGGAGATTTATTTGCTTTTTACTTTTTACGTTTTGCGAATA	TTTCATTCAACTGTGGTAGCCGAATTAATCGTGTTTCATTCA	10010	10090   10100   10110   10120   10130   10140   10150   10140   1015	10160 10170 10180 10190 10200 10210 10220 GTAACACATTTCACTAACACATTTACTAACAACCAGACTCTGGGCCTGTTAATTTTTTAATAGAAATTTT	10230 10240 10250 10260 10270 10280 10290  AAGICCTCAITITCTITCGTGITITITIAAGCTTAATITITICTGGCTTTAITCATAAATITCTTAAGGTCAAC	10300 10310 10320 10330 10340 10350 10360  TACATITGAAAATCAAAGACCTGCAITTTAAATICTTATTCACCTCTGGCAAAACCATTCACAAACCATGG TACATITGAAAAATCAAAGACCTGCATTTAAATTCTTATTCACCTCTGGCAAAACCATTCACAAAACCATGG TACATTTGAAAAATCAAAAACCATTTAAATTCTTATTCACCTCTGGCAAAACCATTCACAAAACCATGG 10300 10310 10320 10320	10370         10380         10400         10410         10420         10430         10440           TAGTABAGGGACACCCTGGCCCATAGGTAAATGTACCACCGTGACCAGGAGATGCAG           TAGTABAGGAGGGGCATAGGTAAATGTACCACGGTGACCCGGTGACCAGGATGCAG           TAGTABAGGAGGACCACGGTGGCCATAGGTAAATGTACCACGGTGACCCGGTGACCAGAGATGCAG           10390         10400         10410         10420         10430         10440	10450 10460 10470 10480 10490 10500 10510 CGCTGAGGGTTTTCCTGAAGGAATAAAGAATGGGTGGAGGGGCGTGCACTGGAAATCACTTGTAGA [	10520 10530 10540 10550 10560 10570 10580 GAAAAGCCCCTGAAAATTTGAGAAAACAAGAACTTACTTA	10590         10610         10620         10630         10650           GCCATTGCTGAGCTGCCTGAACTGGGAACAACAACAACAACCACTCTGATAATCATTGAGTCAA         GCCATTGCTGGTGTGAGTGAGAACAACAACAACAACAACTCTGATAATCATTGAGTCAA           10590         10610         10610         10630         10630         10650
--	--	-------	--	--	---	---	---	--	--	--

	GRACAGCAGCAGTGATTGAGGAGTGAGAGGTACAGGCCAAAATTCTTATCTTGATTATATTATATGTCTGAGGAGTACAGGCCCAAAATTCTTATCTTGATTATATTATATGTCTGAGGCCAAAATTCTTATGTTGATTATATTATATGTCTGAGGCCAAAATTCTTATGTTGATTATATTATATGTCTTGTTGATTATATATGTCTTGTTGTTATATGATTATGTTGTTGTTATATGATTATGTTGT	GGTACAGGCCAA	AAAATTCTTA	TGTTGTAT	TATAATATI 
GrcArr 10670	GTACAGCAGGTGATTGAGGACTGCTGAGAGGCAAAAATTCTTATGTTTGTATAATAATGTCATG 0660 10670 10680 10690 10700 10710 10720	GGTACAGGCCAA	AAAATTCTTA 10700	TGTTGTAT 10710	TATAATAATG 10720
10740 'ACTGTCAG'          'ACTGTCAG'	30	0 10770 CTTCACAAACTC              CTTCACAAACTC 0 10770	rcacacac          rcacacac	10780 ACATTTAAAA            ACATTTAAAA	10790 ACAAAACACT           ACAAAACACT
10810 TCCCCAAATT          TCCCCAAATT	10810 10820 X TAAAATCCCCAAATTTTTCATAAAC				

```
Init. Opt.
Length Score Score Sig. Frame
                                                                                       Results file us-09-497-957-9.res made by tport on Fri 17 Jun 105 18:01:23-PST.
                                                                                                                                                                               Results of the initial comparison of US-09-497-957-9 (1-1440) with: Pile : US09497957.seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30
500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Standard Deviation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total Elapsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A 100% identical sequence to the query sequence was found:
                                                                                                                            Query sequence being compared:US-09-497-957-9 (1-1440)
Number of sequences searched: 70
Number of scores above cutoff: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-tuple
Joining penalty
Window size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The scores below are sorted by initial score. Significance is calculated based on initial score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEARCH STATISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Median
19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       51359
70
70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PARAMETERS
                                                PastDB - Fast Pairwise Comparison of
Release 5.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            00:00:00:00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unitary
1
5.00
0.33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Number of residues:
Number of sequences searched:
Number of scores above cutoff:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mean
143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Description
 320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence Name
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scores:
<u>00</u>0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Times:
                                                                                                                                                                                                                                               252000
                                                                                                                                                                                                                                                                                                                                                                             OMODMEDMO
```

000 | 150 | 160 | 170 | 180 | 190 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 | 210 3.61 3.61 11 0 a above mean \*\*\*\*

1440 1439 1439

1440 1438 1438 Init. Opt. Length Score Score 1440 1440 1440 Optimized Score = 1440 Significance 100% Matches = 1440 Mismatches 0 Conservative Substitutions 1440 1. US-09-497-957-9 (1-1440) US-09-497-957-9 Sequence 9, Application US/09497957 1. US-09-497-957-9 Sequence 9, Application US \*\*\*\* 3 standard deviations 2. US-09-497-957-11 Sequence 11, Application 3. US-09-497-957-10 Sequence 10, Application 4. US-09-497-957-12 Sequence 12, Application other best scores is: Description Initial Score = Residue Identity = Gaps Sequence Name The list of

п

Conservative Substitutions

0

n

	### ##################################	940 950 960 970 980 1000  GGCTGAAGGATAAGCAGCCAATGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGA  GGCTGAAGGATAAGCAGCCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGGATGGGA  GGCTGAAGGATAAGCAGCCCAATGGATGCCAAGGAGTTCGAACCTAAAGACGTATTGCCCAATGGGATGGGA  940 950 1000 1020 1030 1040 1050 1060 1070 1080  CCTACCAGGGCTGGATAACCTTGGCTGTACCCCTGGGGAAGAGCAGAATAACGTGCCAGGTGGAGCACC  CTACCAGGGCTGGATAACCTTGGCTTGTACCCCTGGGGAAGAGAGAATAACGTGCCAGGTGGACCCCTGGGGAAGAGAGAAGAGAATAACGTGCCAGGTGGACCCCTGGGGAAGAGAGAATAACGTGCCAGGTGGACCCCTGGGGAAGAGAAGAGAAAATAACGTGCCAGGTGGCACCC  1010 1020 1030 1040 1050 1060 1070 1080	1090	1230   1240   1250   1260   1270   1280   1290
--	--	--	------	--

Significance Mismatches (1-1440) Sequence 11, Application US/09497957 Optimized ( Matches 1439 99**%** US-09-497-957-9 ( US-09-497-957-11 Initial Score Residue Identity

3.61 n 11

1439 1439

0 11

Score

H 9

| 310 | 310 | 350 | 360 | 310 | 320 | 340 | 350 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 | 360 630 620 610 900 590 580

220 2 GGGAAATGGGCC 	290 290 GCTTGCTGGTT 	370 370 TTGAAGCTTTGG 	440 GAACTCCATGGG [	510 S10 ATCACATGITCA 	580 580 AGGICAICCING            AGGICAICCING 580	650 650 AGACCACCTTG 	730 730 TCGAGTGGGAAA 	800 TGCAGCAGTTGC           TGCAGCAGTTGC 800	70 3ACCTCT         3ACCTCT 70	940 GGCTGAAGGATA           GGCTGAAGGATA 940	1010 CCTACCAGGGCT 
# # # # # # # # # # # # # # # # # # #	940 950 960 970 980 1000 GGTTGAAGGATAACAGCCAATGCCAATGCCAAGAATTCCAACCTAAAGACTATTGCCCAATGGCAATGGGAAAGAGAATTCCAACTAATGCCCAATGGGAATGGAAAGAATGCAATGCCCAATGGCAATGAATG	1010         1020         1030         1040         1050         1060         1070         1080           CCTACCAGGGCTGGATGCTGTACCCCCTGGGGAAGAGAATATACGTGCCAGGTGGACACC	1090 1100 1110 1120 1130 1140 1150 CAGGCCTGGATCAGCCCTCATTGTGATCTGGGAGCCCTCACCGTCTGGCACCCTAGTCATTGGAGTCATCA	. 1160 1170 1180 1200 1210 1220 GTGGAATTGCTGTTTTTGTTCATTGGAATTTTGTTCATAATATTAAGGAAGACGCAGGGTT	1230 1240 1250 1260 1270 1280 1290 CAAGAGGAGCCATGGGCACTACGTCTTAGCTGAACGTGACACGCCTGCAGACTCACTGTGGGAA	1300	1370	3. US-09-497-957-9 (1-1440) US-09-497-957-10 Sequence 10, Application US/09497957 Initial Score = 1439 Optimized Score = 1439 Significance = 3.61 Residue Identity = 99% Matches = 1439 Mismatches = 1 Gaps = 0 Conservative Substitutions = 0	X 10 20 30 40 50 60 70 GGGGACACTACACAGCAGCAGCACTACTCTCTCTCTCTCT	80  AAAGACCTGTTGCTTCACCAGGAAGTTTTACTGGGCATCTCCTGAGCCTAGGCAATAGCTGTAGGGTGAC	150 160 170 180 210 TTTGGAGCCATCCCCGTTTCCCGGCCCCCCAAAGAAGAGCGGAATTTAACGGGGACTGCGGCCAGAGCTG

) 190 200 210	260 270 280  TCCTGATGCTTTTGCAGACGCGGTCCTGCAGGGGC	330 340 350 360 360 160 350 160 350 160 350 160 350 160 350 160 330 160 350 160 350 160 350 160 350 160 350 360 360 360 360 360 360 360 360 360 36	400 410 420 430 430 100 420 430 100 430 100 430 100 100 100 100 100 100 100 100 100 1	470	550 560 570  MARANTCACAACCAAGGAGTCCCACACCCTGC	620 GTACCGAGGGCTACTGGAAGTACGGGTATCATGGGC 	720 700 710 720 720 720 720 720 720 720 720 720 720	780 790 790 790 790 790 790 790 790 790 79	130   840   850   860   860   860   860   860   860   860   860   860   860   860   860   850   850   860   850   860   850   860	910 920 9CCTTGAACTACCCCCGGAACATCACCATGAAGT 	980 1000 TCGAACCTAAAGACGTATTGCCCAATGGGA 	1050 1060 1060 1070 1080 1070 1080 1070 1080 1070 1080 1070 1080 108
150 160 170 180	220 230 240 250 GGGAAATGGGCCGCGAGCCAGGCCGCGCTTCTCCTC	290 300 310 GCTTGCTGCGTTCACACTCTCTGCATACTTCATA 	370 380 390 390	440 450 460 470 GAACTCCATGGGTTTCCAGTAGAATTTCAAGCCAGATG	510 520 530 540 51 ATCACATGTTGACTTCTGGACTATTATGGAAAATCACI	580 610 AGGTCATCCTGGGCTGTGAAATGCAAGAAGAAAAGGTAC	650 660 670 680 690 AGGACCACCTTGAATTCTGCCCTGACACACTGGATTGGAGAGC	730 TGGAGTGGGAAAGCACAAGATTCGGGCCAGGAAATTCGGGCCAGGAAAGCAAAGATTCGGCCAGGCAGAAATTCGGCCAGGCAGAAATTCGGCCAGGCAGG	810 810 820 830 TGCAGCACTTGCTGGAGCTGGGGAGAGGTGTTTTCGACC	870 ATGRACTETT CAGTCA CCACTCTACGETGT CGGGCCT	940 GGCTGAAGGATAAGCAGCCAATGGATGCCAAGGAGTTCC 	1010 1020 1030 CCTACCAGAGATAACCTTGGCTGTACCCCTGGC

430	500 rgaaagggrggg            rgaaagggrggg 500	570 CCACACCTGC            CCACACCTGC 570	ATGATGGGC	720 CCACCAAGC          CCACCAAGC 720	790 CTGCACAGC           CTGCACAGC 790	860 AGTGACACATC             AGGTGACACATC 860	SCATGAAGT             CCATGAAGT	GGGATGGGA            	1080 CCAGGTGGAGCACC               CCAGGTGGAGCACC CCAGGTGGAGCACC	1150 GGAGTCATCA           GGAGTCATCA	1210 TAATRITAAGGAAGAGCAGGGTT 	290 CTGTGGGAA           CTGTGGGAA
420	490 CAGAGTCTGAJ           CAGAGTCTGAJ 490	560   ACAGCAAGGAGTCCC 	630 GCTACTGGAAGTACGGGTATGATG                    GCTACTGGAAGTACGGGTATGATG 630 6410	0 680 690 700 710  CTGACACACTGGATTGCAGAGCAGCAGACCCAGGCCTTGGCC	$\omega - \omega$	850 CTTTGGTGAAGG              CTTTGGTGAAGG	920 CCCCCAGACATCACCATGAAGT 	1000 rrgcccaargggga1 	1070 acgreccage:           acgraccage: 1070	1140 ACCCTAGTCATTG             ACCCTAGTCATTG	1210 FTAAGGAAGA( FTAAGGAAGA( 1210	1260 CTGAACGTGAGTGACACGCAGCTTGCAGACTCACTV CTGAACGTGAGTGACACGCCTGCAGACTCACTV CTGAACGTGAGTGACACGCAGCTTGCAGACTCACTV CTGAACGTGAGTGACACGCAGCTTGCAGCTTGAGCTGAGCTTGAGCTGAGCTTGAGCTGAGCTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCAGCTGAGCAGCTGAGCAGCTGAGCAGCTGAGCAGCTGAGCAGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
410	480 CAGCTGAGT          CAGCTGAGT	550 CAACCACAGG             CAACCACAGGG	63( 3GGCTACTGGA            3GGCTACTGGA	700 AGCAGAACCC            AGCAGAACCC	50 CAGGCAGAACAGGCCTACCTGGAGAGGGACTGC 	된그런	CACTA CACTA CACTA	980 ACCTARAGACGTATTGCCC.               ACCTARAGACGTATTGCCC.	030 1040 1050 1060 1) CTTGGCTGTACCCCCTCGGGAAAAGCAGAATATACGTGC	1130 CCTCTGCACC             CCGTCTGCACC	1200 STTCATAATA: 	270 1.3 ACACGCAGCCT            ACACGCAGCCT 270 1.3
400	470 CCAGATGTGGCTG(            CCAGATGTGGCTG( 470	5 <u>=</u> 5	620 ACAGTACCGAGGGC               ACAGTACCGAGGGC	690 ATTGGAGAGCA            ATTGGAGAGCA 690	760 AGAACAGGGCC            AGAACAGGCC 760	830 CGACCAACAAGTGCC 	890 900 CCACTTAGGGTGTGGGGCCTTGAACT	<b>∡</b> —∡	1050 TIGGGGAAGA(           TIGGGGAAGA(	120 120 120 120 120 120 120 120 120 120	1190 PTGGAATTTTC 	260 12 AACGTGAGTGA            AACGTGAGTGA
390	460 TTTCAAGCCA             TTTCAAGCCA	520 CACTGTTGACTTCTGGACTATTATGGAAAA 	610 PAGAAGACA           PAGAAGACA	680 HCACACTGGI HHHHH BACACACTGGI	750 :GGCCAGGCZ           :GGCCAGGCZ 750	800 810 820 830 820 830 8410 8410 8410 8410 8410 8410 8410 841	190 TACGGTGTCC            TACGGTGTCC	970 ATGCCAAGGAGTTCG              ATGCCAAGGAGTTCG	1040 SCTGTACCCCC           SCTGTACCCC	1100 1110 CCTCATTGTGAAGCCC [	1180 	150 17 STCTTAGCTGA            STCTTAGCTGA
380	40 CATGGTTTCAGTAGAATTTAAGC 	20 5 GTTGACTTCT           GTTGACTTCT	600 TGTGAAATGC           TGTGAAATGC	670 Trerecere           Trerecere	730 740 750 750 750 750 750 750 750 750 750 75	810 GAGCTGGGGA H         GAGCTGGGGA 810	60 GTGACCACTC GTGACCACTC GTGACCACTC	960 CAGCCAATGGATGCC 	1030 IATAACCTTGC 	1100 CCCCTCATTG           CCCCTCATTG	1170 TTTGTCGTCF             TTTGTCGTCF	40 GGGCACTACG           GGGCACTACG
370	440 CTCCATGGGTT            CTCCATGGGTT 440	510 ATCACATGTTCACT             ATCACATGTTCACT 510	590 600 610 FORTCTGGGAAAGGAAGGAAGGAAGGAAGGAAGGAAGGAAGGA	660 670 CCACCTTGAATTCTGCCC	730 \GTGGAAAGG           \GTGGGAAAGG 730	800 CAGCAGTTGCTG            CAGCAGTTGCTG 800	170 880 IGACCTCTTCAGTGACC 	940 GGCTGAAGGATAAGCAGC 	1020 10 ACCAGGGCTGGATAACC               ACCAGGGCTGGATAACC 1020 10	1090 SCTGGATCAGCCCC               SCTGGATCAGCCCC	1160 1170 1180 1190 1200 Gresaarrecrerritarrerrerrerrerrerrerrerrerrerrerrerrerre	1230 CAAGAGGCCATGGGGCACTACGTCTTAGG 
	GAAC       BAAC	ATC ATC ATC	580 AGGTC 	650 AGGAC       AGGAC 650	TGGAG7 	70-17 83-17 83-18	870 ATGTGAC         ATGTGAC 870	246 246 246 246 246 246	1010 CCTACC         CTACC	cagg(       cagg(	6766        -	CAAC 

	TGAACCT	177451	×	TTCCCCA	<u>=</u>	TTCCCCA	1440
1360	GGAGAGAGT	1360	1430	CAAAAAGAT	<u>=</u>	CAAAAAGAT	1430
1350	CATGTTTCA	1350	1420	<b>TTCATTTCCT</b>	= = =	FTCATTTCCT	1420
1340	ATGAGCTCT:	1340	1410	CCTTCTCTG		CCTTCTCTG	1410
1330	GGAGACAAAACTAGAGACTCAAAGAGGGAGTGCATTTATGAGCTCTTCATGTTTCAGGAGAGAGA	1330	1400	aaacatagaaattgcctgacgaactccttgattttagccttctctgttgttcttctcataaaaagatttcccca		aaacatagaaattgcctgacgaactccttgatttttagccttctgttctctttcctcaaaaagatttccca	1400
1320	CTCAAAGAGG	1320	1390	GACGAACTCC	= = = =	GACGAACTCC	1390
1310	AAACTAGAGA 	1310	1380	GAAATTGCCT	= = = =	GAAATTGCCT	1380
1300	GGAGACA 	1300	1370	AAACATA	= = =	AAACATA	1370

THIS PAGE IS BLANK